Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for treating HIV infection in a human infected with the HIV virus, ~~wherein HIV entry into an immune cell is facilitated by a CCR5 receptor,~~ said method comprising:

[[~~a~~)]] transplanting into the human a stem cell-rich population of cells from a human donor, wherein the stem cell-rich population of cells has been screened to identify that it has a beneficial gene that has ~~is~~ a homozygous polymorphism in a CCR5 gene and the encoded CCR5 receptor does not facilitate HIV entry into the immune cell, wherein in the polymorphism is a 32 basepair deletion in the coding region of the CCR5 gene ~~or a CCR5m303 mutant~~, and wherein the immune cells of the ~~said~~ human are reduced or eliminated prior to transplantation, thereby treating the ~~said~~ HIV infection, wherein HIV entry into the immune cell of the ~~said~~ human is facilitated by the CCR5 receptor and wherein the stem cell-rich population of cells is umbilical cord blood.

2-19 (Canceled)

20. (Previously presented) The method of claim 1, wherein said method further comprises identification of the HLA genotype or phenotype of said stem cell-rich population of cells.

21-23 (Canceled)

24. (Previously presented) The method of claim 1, further comprising a step of screening a cell sample from a human donor to identify the stem cell-rich population of cells that has a polymorphism in the CCR5 gene.

25. (Previously presented) The method of claim 24, wherein said polymorphism in the CCR5 gene is detected using a hybridization-based assay, a sequencing assay, or a functional assay.

26-27 (Canceled)

28. (Previously presented) The method of claim 24, wherein said method further comprises

b) identification of an HLA genotype or phenotype of said stem cell-rich population of cells.

29. (Previously presented) The method of claim 28, wherein said identification of the HLA genotype is via a high-throughput method using allele-specific primers and HLA locus-specific capture oligonucleotides immobilized on a solid phase.

30. (Previously presented) The method of claim 28, wherein said method further comprises

c) identification of an HLA genotype or phenotype of said human.

31. (Previously presented) The method of claim 28, wherein said HLA genotype or phenotype of said stem cell-rich population of cells is compatible with said HLA genotype or phenotype of said human.

32. (Canceled)

33. (Previously presented) The method of claim 1, wherein multiple samples of the stem cell-rich populations of cells with the beneficial gene are transplanted into the human.

34. (Previously presented) The method of claim 33, wherein the multiple samples of the stem cell-rich populations of cells with the beneficial gene have an HLA unmatched genotype or phenotype.